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SEQUENCE LISTING

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Blumwald, Eduardo

<120> IMPROVED TRANSPORTERS AND THEIR USES

<130> 023070-127310US

<140> US 10/520,497

<141> 2003-07-09

<150> WO PCT/US2003/021549

<151> 2003-07-09

<150> US 60/395,662

<151> 2002-07-12

<160> 22

<170> PatentIn version 3.3

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<211> 1614

<212> DNA

<213> Arabidopsis thaliana

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 <211> 538  
 <212> PRT  
 <213> Arabidopsis thaliana

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20 25 30

Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn Glu  
35 40 45

Ser Ile Thr Ala Leu Leu Ile Gly Leu Gly Thr Gly Val Thr Ile Leu  
50 55 60

Leu Ile Ser Lys Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp  
65 70 75 80

Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe  
85 90 95

Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu  
100 105 110

Phe Gly Ala Val Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly  
115 120 125

Val Thr Gln Phe Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly  
 130 135 140

Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys  
 145 150 155 160

Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu  
 165 170 175

Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val Val Phe  
 180 185 190

Asn Ala Ile Gln Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala  
 195 200 205

Phe His Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu  
 210 215 220

Leu Gly Ala Ala Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu  
 225 230 235 240

Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu  
 245 250 255

Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly  
 260 265 270

Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp  
 275 280 285

His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala  
 290 295 300

Thr Leu Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met  
 305 310 315 320

Asp Ala Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly  
 325 330 335

Thr Ser Ile Ala Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly  
 340 345 350

Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys  
 355 360 365

Lys Asn Gln Ser Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp  
 370 375 380

Trp Ser Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn  
 385 390 395 400

Lys Phe Thr Arg Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met  
 405 410 415

Ile Thr Ser Thr Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly  
 420 425 430

Met Leu Thr Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala  
 435 440 445

Thr Thr Ser Met Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile  
 450 455 460

Pro Leu Leu Asp Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn  
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Val Pro Arg Pro Asp Ser Ile Arg Gly Phe Leu Thr Arg Pro Thr Arg  
 485 490 495

Thr Val His Tyr Tyr Trp Arg Gln Phe Asp Asp Ser Phe Met Arg Pro  
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Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn Glu  
 35 40 45

Ser Ile Thr Ala Leu Leu Ile Gly Leu Gly Thr Gly Val Thr Ile Leu  
 50 55 60

Leu Ile Ser Lys Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp  
 65 70 75 80

Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe  
 85 90 95

Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu  
 100 105 110

Phe Gly Ala Val Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly  
 115 120 125

Val Thr Gln Phe Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly  
 130 135 140

Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys  
 145 150 155 160

Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu  
 165 170 175

Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val Val Phe  
 180 185 190

Asn Ala Ile Gln Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala  
 195 200 205

Phe His Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu  
 210 215 220

Leu Gly Ala Ala Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu  
 225 230 235 240

Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu  
 245 250 255

Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly

260

265

270

Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp  
 275 280 285

His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala  
 290 295 300

Thr Leu Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met  
 305 310 315 320

Asp Ala Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly  
 325 330 335

Thr Ser Ile Ala Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly  
 340 345 350

Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys  
 355 360 365

Lys Asn Gln Ser Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp  
 370 375 380

Trp Ser Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn  
 385 390 395 400

Lys Phe Thr Arg Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met  
 405 410 415

Ile Thr Ser Thr Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly  
 420 425 430

Met Leu Thr Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala  
 435 440 445

Thr Thr Ser Met Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile  
 450 455 460

Pro Leu Leu Asp Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn  
 465 470 475 480

Val Pro Arg Pro Asp Ser Ile Arg Gly Phe Leu Thr Arg Pro Thr Arg  
 485 490 495

Thr Val His Tyr Tyr Trp Arg Gln Phe Asp Asp Cys Phe Met Arg Pro  
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Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn Glu
          35           40           45

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Ser Ile Thr Ala Leu Leu Ile Gly Leu Gly Thr Gly Val Thr Ile Leu
          50           55           60

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Leu Ile Ser Lys Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp
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Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe
          85           90           95

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Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu
          100          105          110

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Phe Gly Ala Val Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly
          115          120          125

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Val Thr Gln Phe Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly
          130          135          140

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Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys
145          150          155          160

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Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu  
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Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val Val Phe  
 180 185 190

Asn Ala Ile Gln Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala  
 195 200 205

Phe His Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu  
 210 215 220

Leu Gly Ala Ala Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu  
 225 230 235 240

Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu  
 245 250 255

Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly  
 260 265 270

Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp  
 275 280 285

His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala  
 290 295 300

Thr Leu Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met  
 305 310 315 320

Asp Ala Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly  
 325 330 335

Thr Ser Ile Ala Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly  
 340 345 350

Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys  
 355 360 365

Lys Asn Gln Ser Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp  
 370 375 380

Trp Ser Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn  
 385 390 395 400

Lys Phe Thr Arg Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met  
 405 410 415

Ile Thr Ser Thr Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly  
 420 425 430

Met Leu Thr Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala  
 435 440 445

Thr Thr Ser Met Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile  
 450 455 460

Pro Leu Leu Asp Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn  
 465 470 475 480

Val Pro Arg Pro Asp Ser Ile Arg Gly Phe Leu Thr Arg Pro Thr Arg  
 485 490 495

Thr Val His Tyr Tyr Trp Arg Gln Phe Asp Asp Ser Phe Met Arg Pro  
 500 505 510

Val Phe Gly Gly Arg Gly Phe Val Pro  
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<220>  
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Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn Glu  
 35 40 45

Ser Ile Thr Ala Leu Leu Ile Gly Leu Gly Thr Gly Val Thr Ile Leu  
 50 55 60

Leu Ile Ser Lys Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp  
 65 70 75 80

Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe  
 85 90 95

Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu  
 100 105 110

Phe Gly Ala Val Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly  
 115 120 125

Val Thr Gln Phe Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly  
 130 135 140

Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys  
 145 150 155 160

Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu  
 165 170 175

Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val Val Phe  
 180 185 190

Asn Ala Ile Gln Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala  
 195 200 205

Phe His Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu  
 210 215 220

Leu Gly Ala Ala Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu  
 225 230 235 240

Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu  
 245 250 255

Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly  
 260 265 270

Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp  
 275 280 285

His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala  
 290 295 300

Thr Leu Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met  
 305 310 315 320

Asp Ala Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly  
 325 330 335

Thr Ser Ile Ala Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly  
 340 345 350

Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys  
 355 360 365

Lys Asn Gln Ser Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp  
 370 375 380

Trp Ser Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn  
 385 390 395 400

Lys Phe Thr Arg Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met  
 405 410 415

Ile Thr Ser Thr Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly  
 420 425 430

Met Leu Thr Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala  
 435 440 445

Thr Thr Ser Met Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile  
 450 455 460

Pro Leu Leu Asp Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn  
 465 470 475 480

Val Pro Arg Pro Asp Ser Ile Arg Gly Phe Leu  
 485 490

<210> 9  
 <211> 1362  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Modified AtNHX1 DL-3.

<400> 9  
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 gaagagaata gatggatgaa cgaatccatc accgccttgt tgattgggct aggcactggt 180  
 gttaccattt tgttgattag taaaggaaaa agctcgcac ttctcgtctt tagtgaagat 240

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cttttcttca tataatctttt gccaccatt atattcaatg cagggtttca agtaaaaaag 300
aagcagtttt tccgcaattht cgtgactatt atgctttttg gtgctgttgg gactattatt 360
tcttgacaaa tcatatctct aggtgtaaca cagttcttta agaagttgga cattggaacc 420
tttgacttgg gtgattatct tgctattggg gccatatthg ctgcaacaga ttcagtatgt 480
acactgcagg ttctgaatca agacgagaca cctttgctth acagtcttgt attcggagag 540
gggtgttgtga atgatgcaac gtcagttgtg gtcttcaacg cgattcagag ctttgatctc 600
actcacctaa accacgaagc tgcttttcat cttcttgga acttcttgta tttgtttctc 660
ctaagtacct tgcttgggtc tgcaaccggg ctgataagtg cgtatgttat caagaagcta 720
tactttggaa ggcactcaac tgaccgagag gttgccctta tgatgcttat ggcgtatctt 780
tcttatatgc ttgctgagct tttcgacttg agcggatatcc tcaactgtgtt tttctgtggg 840
attgtgatgt cccattacac atggcacaat gtaacggaga gctcaagaat aacaacaaag 900
catacctttg caactttgtc atttcttgcg gagacattta ttttcttgta tgttggaatg 960
gatgccttgg acattgacaa gtggagatcc gtgagtgaca caccgggaac atcgatcgca 1020
gtgagctcaa tcctaattggg tctggatcatg gttggaagag cagcgttcgt ctttccgtta 1080
tcgtttctat ctaacttagc caagaagaat caaagcgaga aaatcaactt taacatgcag 1140
gttgatgattt ggtgggtctgg tctcatgaga ggtgctgtat ctatggctct tgcatacaac 1200
aagtttacaa gggccgggca cacagatgta cgcgggaatg caatcatgat cagagtagc 1260
ataactgtct gtcttttttag cacagtgggtg tttggtagtc tgaccaaacc actcataagc 1320
tacctattac cgcaccagaa cgccaccacg agcatgttat ct 1362

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<210> 10
<211> 454
<212> PRT
<213> Artificial

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<220>
<223> Putative amino acid encoded by modified AtNHX1 DL-3.
<400> 10

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Met Leu Asp Ser Leu Val Ser Lys Leu Pro Ser Leu Ser Thr Ser Asp
1           5           10           15

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His Ala Ser Val Val Ala Leu Asn Leu Phe Val Ala Leu Leu Cys Ala
          20           25           30

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Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn Glu
          35           40           45

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Ser Ile Thr Ala Leu Leu Ile Gly Leu Gly Thr Gly Val Thr Ile Leu  
 50 55 60

Leu Ile Ser Lys Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp  
 65 70 75 80

Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe  
 85 90 95

Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu  
 100 105 110

Phe Gly Ala Val Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly  
 115 120 125

Val Thr Gln Phe Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly  
 130 135 140

Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys  
 145 150 155 160

Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu  
 165 170 175

Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val Val Phe  
 180 185 190

Asn Ala Ile Gln Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala  
 195 200 205

Phe His Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu  
 210 215 220

Leu Gly Ala Ala Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu  
 225 230 235 240

Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu  
 245 250 255

Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly  
 260 265 270

Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp  
 275 280 285

His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala



290

295

300

Thr Leu Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met  
305 310 315 320

Asp Ala Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly  
325 330 335

Thr Ser Ile Ala Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly  
340 345 350

Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys  
355 360 365

Lys Asn Gln Ser Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp  
370 375 380

Trp Ser Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn  
385 390 395 400

Lys Phe Thr Arg Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met  
405 410 415

Ile Thr Ser Thr Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly  
420 425 430

Met Leu Thr Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala  
435 440 445

Thr Thr Ser Met Leu Ser  
450

<210> 11  
<211> 1566  
<212> DNA  
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<220>  
<223> Modified AtNHX1 NDL-1 cDNA.

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ctaggcactg gtgttaccat tttgttgatt agtaaaggaa aaagctcgca tcttctcgtc 180  
tttagtgaag atcttttctt catatatctt ttgccacca ttatattcaa tgcagggttt 240  
caagtaaaaa agaagcagtt tttccgcaat ttcgtgacta ttatgctttt tgggtgctgtt 300

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gggactatta tttcttgac aatcatatct ctaggtgtaa cacagttctt taagaagttg 360
gacattggaa cctttgactt gggtgattat cttgctattg gtgccatatt tgctgcaaca 420
gattcagtat gtacactgca ggttctgaat caagacgaga cacctttgct ttacagtctt 480
gtattcggag aggggtgttg gaatgatgca acgtcagttg tggctctcaa cgcgattcag 540
agctttgatc tcaactcacct aaaccacgaa gctgcttttc atcttcttgg aaacttcttg 600
tatttgtttc tcctaagtac cttgcttggt gctgcaaccg gtctgataag tgcgtatggt 660
atcaagaagc tatacttttg aaggcactca actgaccgag aggttgccct tatgatgctt 720
atggcgatc tttcttatat gcttgotgag cttttcgact tgagcgggat cctcaactgtg 780
tttttctgtg gtattgtgat gtcccattac acatggcaca atgtaacgga gagctcaaga 840
ataacaacaa agcatacctt tgcaactttg tcatttcttg cggagacatt tattttcttg 900
tatgttgcaa tggatgcctt ggacattgac aagtggagat ccgtgagtga cacaccggga 960
acatcgatcg cagtgaagtc aatcctaag ggtctgggtc tggttggaag agcagcggtc 1020
gtctttccgt tatcgtttct atctaactta gccagaaga atcaaagcga gaaaatcaac 1080
ttaacatgc aggttgtgat ttggtggtct ggtctcatga gaggtgctgt atctatggct 1140
cttgcataca acaagtttac aaggggccggg cacacagatg tacgcgggaa tgcaatcatg 1200
atcacgagta cgataactgt ctgtcttttt agcacagtgg tgtttggtat gctgaccaa 1260
ccactcataa gctacctatt accgcaccag aacgccacca cgagcatgtt atctgatgac 1320
aacaccccaa aatccataca tatccctttg ttggaccaag actcgttcat tgagccttca 1380
gggaaccaca atgtgcctcg gcctgacagt atacgtggct tcttgacacg gccactcga 1440
accgtgcatt actactggag acaatttgat gactccttca tgcgaccgt ctttgagggt 1500
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<210> 12
<211> 522
<212> PRT
<213> Artificial

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<220>
<223> Putative amino acid encoded by modified AtNHX1 NDL-1 cDNA.

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<400> 12

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Met Ala Ser Val Val Ala Leu Asn Leu Phe Val Ala Leu Leu Cys Ala
1           5           10          15

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Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn Glu

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20

25

30

Ser Ile Thr Ala Leu Leu Ile Gly Leu Gly Thr Gly Val Thr Ile Leu  
35 40 45

Leu Ile Ser Lys Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp  
50 55 60

Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe  
65 70 75 80

Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu  
85 90 95

Phe Gly Ala Val Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly  
100 105 110

Val Thr Gln Phe Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly  
115 120 125

Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys  
130 135 140

Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu  
145 150 155 160

Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val Phe  
165 170 175

Asn Ala Ile Gln Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala  
180 185 190

Phe His Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu  
195 200 205

Leu Gly Ala Ala Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu  
210 215 220

Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu  
225 230 235 240

Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly  
245 250 255

Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp  
260 265 270

His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala  
 275 280 285

Thr Leu Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met  
 290 295 300

Asp Ala Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly  
 305 310 315 320

Thr Ser Ile Ala Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly  
 325 330 335

Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys  
 340 345 350

Lys Asn Gln Ser Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp  
 355 360 365

Trp Ser Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn  
 370 375 380

Lys Phe Thr Arg Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met  
 385 390 395 400

Ile Thr Ser Thr Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly  
 405 410 415

Met Leu Thr Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala  
 420 425 430

Thr Thr Ser Met Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile  
 435 440 445

Pro Leu Leu Asp Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn  
 450 455 460

Val Pro Arg Pro Asp Ser Ile Arg Gly Phe Leu Thr Arg Pro Thr Arg  
 465 470 475 480

Thr Val His Tyr Tyr Trp Arg Gln Phe Asp Asp Ser Phe Met Arg Pro  
 485 490 495

Val Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro Thr  
 500 505 510

Glu Arg Asn Pro Pro Asp Leu Ser Lys Ala  
 515 520

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 <211> 1410  
 <212> DNA  
 <213> Artificial

<220>  
 <223> NDL-2 cDNA.

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 actattatgc tttttggtgc tgttgggact attatttctt gcacaatcat atctctaggt 180  
 gtaacacagt tctttaagaa gttggacatt ggaacctttg acttgggtga ttatcttgct 240  
 attggtgcca tatttgctgc aacagattca gtatgtacac tgcaggttct gaatcaagac 300  
 gagacacctt tgctttacag tcttgtattc ggagaggggtg ttgtgaatga tgcaacgtca 360  
 gttgtggtct tcaacgcgat tcagagcttt gatctcactc acctaaacca cgaagctgct 420  
 tttcatcttc ttggaaactt cttgtatttg tttctcctaa gtaccttgct tgggtgctgca 480  
 accggtctga taagtgcgta tgttatcaag aagctatact ttggaaggca ctcaactgac 540  
 cgagaggttg cccttatgat gcttatggcg tatctttctt atatgcttgc tgagcttttc 600  
 gacttgagcg gtatcctcac tgtgtttttc tgtggtattg tgatgtccca ttacacatgg 660  
 cacaatgtaa cggagagctc aagaataaca acaaagcata cctttgcaac tttgtcattt 720  
 cttgcggaga catttatattt cttgtatggt ggaatggatg ccttggacat tgacaagtgg 780  
 agatccgtga gtgacacacc gggaacatcg atcgcagtga gctcaatcct aatgggtctg 840  
 gtcatgggtg gaagagcagc gttcgtcttt ccgttatcgt ttctatctaa cttagccaag 900  
 aagaatcaaa gcgagaaaat caactttaac atgcaggttg tgatttggtg gtctgggtctc 960  
 atgagaggtg ctgtatctat ggctcttgca tacaacaagt ttacaagggc cgggcacaca 1020  
 gatgtacgcg ggaatgcaat catgatcacg agtacgataa ctgtctgtct ttttagcaca 1080  
 gtggtggttg gtatgctgac caaaccactc ataagctacc tattaccgca ccagaacgcc 1140  
 accacgagca tgttatctga tgacaacacc ccaaaatcca tacatatccc tttgttgagc 1200  
 caagactcgt tcattgagcc ttcagggaa cacaatgtgc ctcggcctga cagtatacgt 1260  
 ggcttcttga cacggcccac tcgaaccgtg cattactact ggagacaatt tgatgactcc 1320  
 ttcattgcgac ccgtcttttg aggtcgtggc tttgtaccct ttgttccagg ttctccaact 1380  
 gagagaaacc ctctgatct tagtaaggct 1410

<210> 14  
 <211> 470  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Putative amino acid encoded by modified AtNHX1 NDL-2 cDNA.

<400> 14

Met Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp Leu Phe Phe Ile  
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Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe Gln Val Lys Lys  
 20 25 30

Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu Phe Gly Ala Val  
 35 40 45

Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly Val Thr Gln Phe  
 50 55 60

Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly Asp Tyr Leu Ala  
 65 70 75 80

Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys Thr Leu Gln Val  
 85 90 95

Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu Val Phe Gly Glu  
 100 105 110

Gly Val Val Asn Asp Ala Thr Ser Val Val Val Phe Asn Ala Ile Gln  
 115 120 125

Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala Phe His Leu Leu  
 130 135 140

Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu Leu Gly Ala Ala  
 145 150 155 160

Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu Tyr Phe Gly Arg  
 165 170 175

His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu Met Ala Tyr Leu  
 180 185 190

Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly Ile Leu Thr Val

195

200

205

Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp His Asn Val Thr  
 210 215 220

Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala Thr Leu Ser Phe  
 225 230 235 240

Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met Asp Ala Leu Asp  
 245 250 255

Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly Thr Ser Ile Ala  
 260 265 270

Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly Arg Ala Ala Phe  
 275 280 285

Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys Lys Asn Gln Ser  
 290 295 300

Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp Trp Ser Gly Leu  
 305 310 315 320

Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn Lys Phe Thr Arg  
 325 330 335

Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met Ile Thr Ser Thr  
 340 345 350

Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly Met Leu Thr Lys  
 355 360 365

Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala Thr Thr Ser Met  
 370 375 380

Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile Pro Leu Leu Asp  
 385 390 395 400

Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn Val Pro Arg Pro  
 405 410 415

Asp Ser Ile Arg Gly Phe Leu Thr Arg Pro Thr Arg Thr Val His Tyr  
 420 425 430

Tyr Trp Arg Gln Phe Asp Asp Ser Phe Met Arg Pro Val Phe Gly Gly  
 435 440 445

Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro Thr Glu Arg Asn Pro  
 450 455 460

Pro Asp Leu Ser Lys Ala  
 465 470

<210> 15  
 <211> 1323  
 <212> DNA  
 <213> Artificial

<220>  
 <223> NDL-3 cDNA.

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 attggaacct ttgacttggg tgattatctt gctattggtg ccatatttgc tgcaacagat 180  
 tcagtatgta cactgcaggt tctgaatcaa gacgagacac ctttgcttta cagtcttgta 240  
 ttcggagagg gtgttggtgaa tgatgcaacg tcagttgttg tcttcaacgc gattcagagc 300  
 tttgatctca ctcacctaaa ccacgaagct gcttttcata ttcttgaaa cttcttgat 360  
 ttgtttctcc taagtacctt gcttggtgct gcaaccgggc tgataagtgc gtatgttata 420  
 aagaagctat actttggaag gcaactcaact gaccgagagg ttgcccttat gatgcttatg 480  
 gcgtatcttt cttatatgct tgctgagctt ttcgacttga gcggtatcct cactgtgttt 540  
 ttctgtggta ttgtgatgtc ccattacaca tggcacaatg taacggagag ctcaagaata 600  
 acaacaaagc atacctttgc aactttgtca tttcttgagg agacatttat tttcttgat 660  
 gttggaatgg atgccttggc cattgacaag tggagatccg tgagtgcac accgggaaca 720  
 tcgatcgcag tgagctcaat cctaattgggt ctggtcatgg ttggaagagc agcgttcgtc 780  
 tttccgttat cgtttctatc taacttagcc aagaagaatc aaagcgagaa aatcaacttt 840  
 aacatgcagg ttgtgatttg gtggtctggt ctcatgagag gtgctgtatc tatggctctt 900  
 gcatacaaca agttttacaag ggccggggcac acagatgtac gcgggaatgc aatcatgata 960  
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 ctcataagct acctattacc gcaccagaac gccaccacga gcatgttatc tgatgacaac 1080  
 accccaaaat ccatacatat ccctttgttg gaccaagact cgttcattga gccttcaggg 1140  
 aaccacaatg tgcctcggcc tgacagtata cgtggcttct tgacacggcc cactcgaacc 1200  
 gtgcattact actggagaca atttgatgac tccttcatgc gacccgtctt tggaggctgt 1260



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gct 1323

<210> 16  
<211> 439  
<212> PRT  
<213> Artificial

<220>  
<223> Putative amino acid encoded by modified AtNHX1 NDL-3 cDNA.

<400> 16

Met Lys Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu Phe  
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Gly Ala Val Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly Val  
20 25 30

Thr Gln Phe Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly Asp  
35 40 45

Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys Thr  
50 55 60

Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu Val  
65 70 75 80

Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Trp Val Phe Asn Ala  
85 90 95

Ile Gln Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala Phe His  
100 105 110

Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu Leu Gly  
115 120 125

Ala Ala Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu Tyr Phe  
130 135 140

Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu Met Ala  
145 150 155 160

Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly Ile Leu  
165 170 175

Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp His Asn  
180 185 190

Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala Thr Leu  
 195 200 205

Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met Asp Ala  
 210 215 220

Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly Thr Ser  
 225 230 235 240

Ile Ala Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly Arg Ala  
 245 250 255

Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys Lys Asn  
 260 265 270

Gln Ser Glu Lys Ile Asn Phe Asn Met Gln Trp Ile Trp Trp Ser Gly  
 275 280 285

Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn Lys Phe Thr  
 290 295 300

Arg Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met Ile Thr Ser  
 305 310 315 320

Thr Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly Met Leu Thr  
 325 330 335

Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala Thr Thr Ser  
 340 345 350

Met Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile Pro Leu Leu  
 355 360 365

Asp Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn Val Pro Arg  
 370 375 380

Pro Asp Ser Ile Arg Gly Phe Leu Thr Arg Pro Thr Arg Thr Val His  
 385 390 395 400

Tyr Tyr Trp Arg Gln Phe Asp Asp Ser Phe Met Arg Pro Val Phe Gly  
 405 410 415

Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro Thr Glu Arg Asn  
 420 425 430

Pro Pro Asp Leu Ser Lys Ala  
435

<210> 17  
<211> 35  
<212> DNA  
<213> Artificial

<220>  
<223> Putative amino acid encoded by modified AtNHX1 NDL-3 cDNA.

<400> 17  
ggagacaatt tgatgactgc ttcattgcgac ccgtc 35

<210> 18  
<211> 35  
<212> DNA  
<213> Artificial

<220>  
<223> Primer SM-23-R

<400> 18  
gacgggtcgc atgaagcagt catcaaattg tctcc 35

<210> 19  
<211> 38  
<212> DNA  
<213> Artificial

<220>  
<223> Primer EXCH-5

<400> 19  
agctaggatc cggatctaga agaagataac aatgttgg 38

<210> 20  
<211> 33  
<212> DNA  
<213> Artificial

<220>  
<223> Primer EXCH-DL-1

<400> 20  
agctgaattc ctaggttaca aagccacgac ctc 33

<210> 21  
<211> 32  
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